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Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein -
                                                                                                                                                                                           Result
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                   Score
80.5
80.5
78.5
78.5
78
78
78
78
78
78
78
78
                                                                                                   85.5
85.5
85
83
83
                                                                                                                                                        522
91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                               SPTREMBL_14:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
                                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                                            10:
12:
13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-373-230-2
808
1 NFGRLHCTTAVIRNINDQVL..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        November 20, 2000, 14:05:47;
 64.6
11.3
10.6
10.5
10.5
10.5
10.3
10.0
10.0
9.9
9.7
9.7
9.7
9.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                     sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                  sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                   Length
 193
987
784
482
483
267
483
267
1039
1196
11196
11196
11196
11196
                                                                                                                                                                                   DB
   Q9Y0A6
073909
Q9XV67
Q29082
Q24892
Q24869
Q9YF27
Q9YF27
Q9RF17
Q45916
Q53550
Q38197
Q9ZX77
                                                                                                                             Q9TU73
Q9V718
Q9V1J4
Q9U9R6
Q9UA14
                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....KKDENGDKSVMFTLTNLHQS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search time 18.88 Seconds (without alignments) 776.469 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297973
Q9tu73 bos taurus
Q9v7i8 drosophila
Q9y1j4 schistosoma
Q9u9r6 schistosoma
Q9ual4 dictyosteli
Q9y0a6 dictyosteli
Q9y0a6 dictyosteli
Q9y0a7 caenorhabdi
Q29082 sus scrofa
Q24892 eimeria max
O84869 chlamydia t
Q9yf27 aeropyrum p
Q9rfi7 streptococc
Q45916 clostridium
Q38197 clostridium
Q9zx77 clostridium
Q9zx77 clostridium
Q9gxmm0 lymantria d
                                                                                                                                                                                     Description
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73	73	73.5	•	•	73.5		•		74		74.5	74.5	74.5	75	75			75.5		~1		76.5	77	77	77.5
9.0	9.0	9.1	9.1	9.1	9.1			_					9.2					9.3			•		•	+	
1298	266	2077	2077	1146	1128	680	647	445	254	950	849	803	661	1146	621	866	818	626	161	525	1294	905	672	563	1631
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044199	Q9TTK1	Q9QJ37	Q9WT33	068317	Q9SAF6	074343	Q02892	Q9XYW4	051029	Q9UN73	Q9Z283	075283	P73025	051778	Q9ZMM2	024295	Q9SHN7	050498	Q62161	Q9UF58	Q9S814	094641	Q9U0K1	Q9SV96	909x606
044199 Caenornabur		/ numan n	numan	Vibrio	arabi	S		Q9xyw4 drosophila			3 mus	homo	P73025 synechocyst			024295 pisum sativ	Q9shn7 arabidopsis	ŲΙ	Q62161 mus musculu	OMO	4	ທ		σ	Q9y6u6 homo sapien

ALIGNMENTS

Q9TU73;
Q9TU73;
Q9TU73;
Q9TU73;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
INTERLEUKIN-18 PRECURSOR.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

QY 119 EGHFLACQKEDDAFKLILKKKDENGDKSVMFTLTN 153 : : : : : : : : : : Db 157 KGYFLACKKENDLFKLILKKQDDNRDKSVMFTVQN 191	
QY 60 AVTLSVKDSKXSTLSCKNKIISFEEMDPPENIDDIQSDLIFFQKRVPGH-NKMEFESSLY 118	н ^
QY 1 NFGRLHCTTAVIRNINDQVLFVDK-RQPVFEDMTDIDQSASEPQTRLIIYMYKDSEVRGL 59 : : :: : : : : : : : : : :	п ^
Query Match 64.6%; Score 522; DB 6; Length 193; Best Local Similarity 65.2%; Pred. No. 1.2e-40; Matches 101; Conservative 30; Mismatches 22; Indels 2; Gaps	
	בים בים בים או
RP SEOUENCE FROM N.A.	ל 112

Q9V718

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RESULT
Q9Y1.J4
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                                                                                                                                                                                                                                                                                                                                                         Db
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                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000
01-MAY-2000
01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G. Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9V7I8;
                                                                              432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG8414 PROTEIN.
                                                                                                                       83
                                                                                                                                                                                                 24 KRQP-VFEDMTDIDQSASEPQTRLIIYMYKDSEVRGLAVTLSVKDSKXSTLSCKNKIISF
               W
                                                                       PEVVTPEKENYLQPSDVPFY--RNPQANPTELSVFENSLKSNHVLAVIKED
                                                                                                               EEMDPPENIDDIQ-SDLIFFQKRVPGHNKME---FESSLYEGHFLACQKED
                                                                                                                                                         QREPLIIEEIFD-DPPVEKKQERIEQSSVMDIVVKNLSSVPPKKESEVAIETEENDEVSL
                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20196006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa; Arthropoda; Tracheata; H
Neoptera; Endopterygota; Diptera;
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                 11.3%;
31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13,
13,
14,
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                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                              Score 91; DB 5; Pred. No. 2.7;
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                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            987 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hexapoda; Insecta;
a; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                              47;
                                                                                                                                                                                                                                                                                      Length 987;
                                                                                                                                                                                                                                              Indels
                                                                         480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zheng L.,
Smith H.O.,
                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                         Gaps
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RESULT
Q9U9R6
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PROSITE; PS00031; NUCLEAR_RECEPT Receptor; Transcription regulatizinc-finger.
SEQUENCE 784 AA; 87249 MW; C
                                                                                                                                                                                                                                 Q9U9R6;
Q9U9R6;
01-MAY-2000 (TrEMBLE
01-MAY-2000 (TrEMBLE
01-JUN-2000 (TrEMBLE
RETINOID-X-RECEPTOR.
                                                       INTERPRO; INTERPRO;
                                                                                                                                       Mendonca
Bonnelye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Y1J4;
Q9Y1J4;
01-NOV-1999
01-NOV-1999
01-MAY-2000
                                                                             homologs.";
Submitted (JUN-1999)
EMBL; AF158102; AAD4
PRINTS;
          PFAM; PF00104; PFAM; PF00105;
                               INTERPRO;
                                          INTERPRO;
                                                                                                                structural and functional
                                                                                                                                                                                    Schistosomatoidea;
                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                            RXR.
Schistosoma
                                                                                                                            "A Schistosoma
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION:
EMBL; AF129816; AAD33428.
INTERPRO; IPR000324; -.
INTERPRO; IPR000536; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mansoni.";
Gene 233:33-38(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-NMRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO; IPR001628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Freebern W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RETINOID X RECEPTOR Schistosoma mansoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                              |: :: | : | : | 513 LVYWLANDHKPRSLSTSNST
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                                                                                                                                                                                                                                                                                                                                                                      FQKRVPGHNKME-FESSLYEGHFLACQKEDDAFKLILKKKDENGDKSVMFTLTNLHQS 157
                                                                                                                                                                                                                                                                                                                                                  INKSVPLDEKMDYYYSNFPE
                                                                                                                                                                                                                                                                                                                                                                                          ... w.J., Niles
a member of t.
PR00047;
                              158102; AAD45325.1; IPR000324; -.; IPR000536; -.; IPR001628; -.; IPR001723; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                       R.L., Escriva H., Bouton D., Vanacker J.-M., Zelus D., E., Pierce R., Laudet V.; cosoma mansoni nuclear receptor of the RXR family shows marked
                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99307140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                Metazoa;
                                                                                                                                                                               mansoni (Blood fluke).
Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
toidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
        hormone_rec; 1.
zf-C4; 1.
STROIDFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . (Bloo
Platy
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27.1
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regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i., Loverde P.T.;
retinoid x receptor family in Schistosoma
                                                                          he
1;
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                                                                                                                                                                                                                                                                                                                                                 FHLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                         %; Score 85.5; DB 5; Length 784; %; Pred. No. 6.6; 18; Mismatches 53; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR (BY SIMILARITY).
                                                                                                             divergence from vertebrate and arthropod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW; CD35E449E5FD547F CRC64;
                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                -- NNLTKPMDNNNNDSISSKPTNINDN 621
                                                                                                                                                                                                                                                                                         784 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         784 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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4.

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RESULT
Q9Y0A6
ID Q9
AC Q9
DT 01
DT 01
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC DIT DOT DOT DOT DOT DOT DOT DOT NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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Best Local
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                discoideum protein phosphatase 2A."; FEBS Lett. 456:7-12(1999).
EMBL; AF138279; AAD29694.1; -.
INTERPRO; IPR000009; -.
INTERPRO; IPR001680; -.
PFAM; PF01240; PR55; 1.
PRINTS; PR00600; PP2APR55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; F
Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UA14 PRELIMINARY; PRT; 482 AA.
Q9UA14;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
PROTEIN PHOSPHATASE 2A 55 KDA REGULATORY B SUBUNIT Dictyostelium discoideum (Slime mold).
Eukaryota; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PROSITE; PS00031; NUCLEAR_RECE
Q9Y0A6 PRELIMINARY;
Q9Y0A6;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 99379588.
Murphy M.B., Levi S.K., Egelhoff T.T.;
"Molecular characterization and immunolocalization of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF01240; PR55; 1.
PRINTS; PR00600; PP2APR55.
PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
PROSITE; PS01024; PR55_1; 1.
PROSITE; PS01025; PR55_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 FQKRVPGHNKME-FESSLYEGHFLACQKEDDAFKLILKKKDENGDKSVMFTLTNLHQS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513 LVYWLANDHKPRSLSTSNSTSKLPDTTPTINSTDISNITDDPPENSISDISKDCTIQMKK 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     573 INKSVPLDEKMDYYYSNFPEFHLL---
                                                                                                                                                                                        133 KLILKKKDENGDKSVMFTL 151
                                                                                                                                                         335 FLTLKLWDINMENKPVKTI 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46
                                                                                                                                                                                                                                                                                                                         14 NINDQVL-FVDKRQPVFEDMTDIDQSASEPQTRLIIYMYKDSEVRGLAVTLSVKDSKXST 72
                                                                                                                                                                                                                                                                                          LIIYMYKDSEVRGLAVTLSVKDSKXSTLSCKNKIISFEEMDPPEN-IDDIQSDLIF---- 100
                                                                                                                                                                                                                          L-CDNHAKVFEEYEDPSNKS----FFSEIISSISDIKFSR---DGRYILSRD----
                                                                                                                                                                                                                                                         LSCKNKIISFEEMDPPENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 AA; 55107 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.6%; Score 85.5; DB 5; Length ilarity 27.1%; Pred. No. 6.6; Conservative 18; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                           10.5%; Score 85; DB lilarity 25.9%; Pred. No. 4.2; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87250 MW;
  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471D4E69EB135A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  95E879E7A37D2392 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----NNLTKPMDNNNNDSISSKPTNINDN 621
                                                                        483 AA.
                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                22;
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O73909 PRELIMINARY; PRT; 26/ AA.
O73909;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
INTERLEUKIN-1BETA.
                                                                                                                                                                                                                                                                                                Weining K.C., Sick C., Kaspers B., Staeheli P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15006; CAA75239.1; -.
HSSP; P18510; 11RA.
INTERPRO; IPRO00975; -.
PFAM; PF00340; interleukin-1; 1.
PROSITE; PS00253; INTERLEUKIN_1; 1.
CHAIN 106 267 INTERLEUKIN-1BETA.
SEQUENCE 267 AA; 29822 MW; 3EF72164E4D40B64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0600; PP2APR55.

PROSITE; PRO0678; WD_REPEATS; UNKNOWN_1.

PROSITE; PS01024; PR55_1; 1.

PROSITE; PS01025; PR55_2; 1.

SEQUENCE 483 AA; 55275 MW; DCF9434FE95C27BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-AX4;
Campanha R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Weining K.C., Sick C
Submitted (SEP-1997)
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Eukaryota; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 KLILKKKDENGDKSVMFTL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 NINTECFNVVDIKPTNMEDLTEVITSAEFHPTSCNIFMYSSSK-----GTIKLGDLRSSA 291
118 DIFDINOKCFVLESPTQLVALHLQGPSSSQKVRLNIALYRPRGPRGSAGTGQMPVALGIK 177
                                                                31 DMTDIDQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSCKNKIISFEEMDPPENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NINDQVL-FVDKRQPVFEDMTDIDQSASEPQTRLIIYMYKDSEVRGLAVTLSVKDSKXST 72
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                                                                                                                                      30;
                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 85; DB 5; Length 483; 25.9%; Pred. No. 4.2; tive 23; Mismatches 58; Indels
                                                                                                                              10.3%; Score 83; DB 13; Length 267; 24.8%; Pred. No. 3.2; :ive 18; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases: 396.1; -.
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of a B regulatory subunit of protein phosphatase
                                                                ----ASEPQTRLIIYMYKDSEVRGLA-----VTLSVK 66
                                                                                                                                        Gaps
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Canaton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Caraton M., Green P., Hawkins T., Hillier L., Jier M., Johnston L.
Cander A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.
Callaghan M.,
Caraton M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Callaghan M.,
Copsey T., Shownkeen
Callaghan M.,
Copsey T.,
Cooper J.,
Coulson
Cooper J.,
Coulson
Callaghan M.,
Copsey T.,
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Best Local S
Matches 55
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01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
F25C8.2 PROTEIN.
F25C8.2.
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Wilson R., Ai
Bonfield J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
EMBL; Z81512; CAB04171.1;
INTERPRO; IPRO02937; -.
PFAM; PF01593; Amino_oxida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F25C8.2.
Caenorhabditis elegans.
Caenorhabditis elegans.
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                                                                            254
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                                                                                                                                                                                                                              NCEVINVKEEEN-
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                                                                                                                                                                                                                                                                  YMYKDSEVRGLAVTLSVKDSKXSTLSCKNKIIS-FEEM--DPPENIDDIQSDLIFFQKRV
                                                                                                                                                                                                                                                                                                                                               GRLHCTTAVIRNINDQV--
                                                                                                                                                                                           PGHNKMEFESSLYEGHFL
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                                                                                                                                                   -NYFQTEWSSPVGELSLSNLSIWDDGTEEEDSAVLNKQGFYEILKDFRSKIPAGNIRL
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94150718.
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                                                                                                                                                                                                                                                                                                                                                                                  10.0%;
nilarity 26.4%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 AA;
                                                                                                              KKDENGDKSVMFTLTN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino_oxidase;
AA; 55505 MW;
                                                                            - IMVTLKNGEVLH
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12,
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                                                                                                                                                                                                                                                                                                                                                                                 Score 81; DB Pred. No. 9.8; Mismatches
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Last sequence up
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172CEC91495557AB CRC64;
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9.8;
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Gene sequence, CDNA construction, expression in Escherichia coli and genetically approached purification of porcine interleukin-1 beta.";

Eur. J. Biochem. 217:45-52(1993).

DR EMBL; X74568; CAA52660.1; -.

DR HSSP; P01584; 1HIB.

DR INTERPRO; IPR000975; -.

DR INTERPRO; IPR002348; -.

DR PFAM; PF00340; interleukin-1; 1.

DR PFAM; PF00340; interleukin-1; 1.

PR PRINTS; PR00262; IL1HBGF.

DR PRINTS; PR00264; INTERLEUKIN1.

PROSITE; PS00253; INTERLEUKIN1.

PROSITE; PS00253; INTERLEUKIN.

QUETV N--
     RESULT
Q24892
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Best Local S
Matches 24
                                                                                                                          Bumstead J.M., Dunn P.P.J
"Nitrocellulose immunoblot cloning of Eimeria maxima proliferation.";
Clin. Diagn. Lab. Immunol
                                                                                                                                                                                                                                                                                                                                                                Q24892;
Q24892;
01-NOV-1996 (TrEMBI
01-NOV-1996 (TrEMBI
01-JUN-2000 (TrEMBI
CALMODULIN-DOMAIN F
 MEDLINE; 9704
Dunn P.P.J.,
"Sequence, ex
                                                                                                                                                                                                                                                                                                                          Eukaryota;
Eimeria.
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Q29082;
01-NOV-1996
01-NOV-1996
01-MAY-2000
                                         STRAIN=HOUGHTON;
MEDLINE; 97048698.
                                                                                      SEQUENCE
                                                                                                                                                                                                                                        MEDLINE;
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Vanderbroeck K.;
Submitted (AUG-1993)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGHNKMEFESSLYEGHFLACQKED 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KNRVEFESALYPNWYISTSQAE 242
                                                                                      FROM N
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Cetar
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      ga CI
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01, Last sequence update)
14, Last annotation update)
IN KINASE (FRAGMENT).
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., Tomley F.M.; localization of calmodulin-domain
                                                                                                                             2:524-530(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 AA.
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Matches 38
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084869;

084869;

01-NOV-1998 (TrEMBLrel. 08, Created)

01-NOV-1998 (TrEMBLrel. 10, Last sequents of the sequents of t
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Parasitology 113:439-448(1996).

EMBL; Z71756; CAA96438.1; -.

HSSP; Q63450; 1A06.

INTERPRO; IPR000719; -.

INTERPRO; IPR002048; -.

INTERPRO; IPR002290; -.

PFAM; PF00036; efhand; 4.

PFAM; PF00069; pkinase; 1.

PROSITE; PS00018; EF_HAND; UNKNOWN_4.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

NON_TER 1 1

SEQUENCE 414 AA; 47427 MW; 780C793F0A45BA68 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 282:754-759(1998).
EMBL; AE001359; AAC68459.1; -.
Hypothetical protein.
SEQUENCE 506 AA; 56464 MW; 4FAA4A12C109ARR4 CDC64.
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Stephens R.S., Kalman S., Lammel C.J.,
Mitchell W.P., Olinger L., Tatusov R.L
Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL 56.5 KDA PROTEIN.
CT861.
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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STRAIN=D/UW-3/CX;
                                                                                                   160 KDNLSPIMEEIDSFSAETESLEERLVTQKKEE 191
                                                                                                                                                                               119 EGHFLACQKEDDAF-
                                                                                                                                                                                                                                                     112 RKLSEKLHFSSELSARDSTKPSSSEPIKPSENL-
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                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                61 VTLSVKDSKXSTLSCKN--KIISFEEMDPPENIDDIQSDLIFFQKRVPGHNKMEFESSLY 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NFGRLHCTTAVIRNINDQVLFVDKRQPVFEDMTDIDQSASEPQTRLIIYMYKDSEVRGLA
                                                                                                                                                                                                                                                                                                                                                                                           SFSRLQPTTP-----KERILFFGS-SPSSQLSSTVRTTTSSPWN-----LFSNSQTRNST 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oh 9.9%; Score 80; DB 2; Similarity 25.0%; Pred. No. 13; 38; Conservative 25; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L., Tatusov R.L., Zhao
                                                                                                                                                                               -KLILKKKDE 141
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Last annotation update)
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                                                                                                                                                                                                                                                     -LHTPEHHK-ELFSSLK 159
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"Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";

DNA Res. 6:83-101(1999).

REMBL; AP000059; BAA79369.1: -

INTERPRO; IPR000330
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Best Local S
Matches 37
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Q9YF27;
Q9YF27;
Q9YF27;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                          Q9RFI7 PRELIMINARY; PRT; 388 AA.
Q9RFI7;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PROTEIN I/II V-REGION (FRAGMENT).
EMBL; AI
              Chatenay-Rivauday C., Yamodo I Klein J.P., Ogier J.; "TNFalpha release by monocytic the extended V-region of the o.J. Leukoc. Biol. 0:0-0(2000). EMBL; AF192472; AAF20187.1; -.
                                                                                                                        SEQUENCE FROM N.A. STRAIN-P4A7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 1039 AA;
                                                                                                                                                                                                                 Streptococcus gordonii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPRO00330; -.
INTERPRO; IPRO01410; -.
INTERPRO; IPRO01650; -.
PFAM; PF00176; SNF2_N; 1.
PFAM; PF00271; helicase_C; 1.
                                                                                                                                                                             Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aeropyrum pernix.
Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                   472
                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 LILKKKDENGDKSVMFTLTN 153
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                                                                                                                                                                                                                                                                                                                                                                                                                LRKWAEDEFGDPGIVRVFTS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KKILGLVLYTPPEELPDEFKDLA-SQKAIVFTEFKDTATYLYE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCKNKIISFEEMDPPENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAFK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMTDIDQSASEPQTRLIIYM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 37; Conser
                                                                                                                                                                                                Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.7%; Score 78.5; Darity 26.4%; Pred. No. 40; Conservative 14; Mismatches
                                                 monocytic THP-1 cells through cross-linking of of the oral streptococcal protein I/II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119959 MW; 30C9191854575F9D CRC64;
                                                                                                      Yamodo I., Sciotti M.A., Troffer-Charlier N.,
                                                                                                                                                                                                Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----YKDSEVRGLAVTLSVKDSKXSTL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1039;
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SO

SEQUENCE

388

AA;

42720

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907F6A76805BCE45 CRC64;

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RESULT
Q45916
ID Q4
AC Q4
DT Q1
DT Q1
DT Q1
DT Q1
CC QC
CC QC
RN C
OC CE
                                                                                                                                                                                                                                                   RESULT
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                                                                                         Q53550 PRELIMINARY;
Q53550;
Q1-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 13, L
01-MAY-2000 (TrEMBLrel. 13, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Hauser D.F., Eklund M.W., Popoff
Submitted (MAY-1992) to the EMBI
SUBMITTER PRO; IPRO00395; -.

INTERPRO; IPRO00395; -.

PFAM; PF01742; Peptidase_M27; 1.

PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; -; 1.

SEQUENCE 1196 AA; 138725 MW;
 PROGENITOR TOXIN L NONT Clostridium botulinum. Bacteria; Firmicutes; B Clostridium.
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Q45916;
Q45916;
Q45916;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
138 KDA PROTEIN ASSOCIATED WITH BONT /C1-HAEMAGGLUTININ COMPLEX.
CHN-138.
Clostridium botulinum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae
Clostridium.
                                                                                                                                                                                                                                                                                                                               1078
                                                                                                                                                                                                                                                                                                                                                                                                                             1024
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Similarity 24.3%;
35; Conservative 23
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27; Conservative
                                                                          WBLrel. 01, Last sequence update)
WBLrel. 13, Last annotation update)
L NONTOXIC-NONHEMAGGLUTININ COMPONENT
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                              Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAFK
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ne EMBL/GenBank/DDBJ
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No. 14;
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                                Clostridiaceae;
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Inoue K., Oguma K.;
"Characterization of r
types of progenitor to
type D CB-16.";
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LSLKNTDGINISSVKFKLII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    f nontoxic-nonhemagglutinin component of the two toxin (M and L) produced by Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.
24.
                                                                                                                                                                                                                                -IDDIOSDLIFFOKRVPGHNKMEFESSLYEGHFLACOKEDDAFK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7%; Score 78; DB 2; Length 1196; 3%; Pred. No. 53; 23; Mismatches 58; Indels
                                                                    NLHQS 157
                                                                                                                                                                                                                                                                                                            KNVANVSIDQILSIYSTNIISLVNKNNSIYVEELSVLDNPI 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujinaga Y., Inoue K., Sunagawa H., Fujii N.,
  NIDES 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             717 MW; 6D2DBB5F6AF38324 CRC64;
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